SEQUENCE LISTING

<110> Joshua Z. Levin
      Ken Phillips
      Greg Budziszewski
      Fred Meins
      Zhenya Glazov

<120> Methods of Controlling Gene Expression

<130> 31481USNP

<140> 09/896,186
<141> 2001-06-29

<150> 60/222,202
<151> 2000-08-01

<160> 34

<170> PatentIn Ver. 2.1

<210> 1
<211> 942
<212> DNA
<213> Arabidopsis thaliana

<400> 1
atgtcatcgt caaattggat cgacgacgct tttacagagg aagagcttct cgctatcgac 60
gccatcgaag cttcctacaa tttctcccgt tcttcttctt cttcttcctc tgctgctccg 120
accgtacaag ctacaacctc cgtccatggc cacgaggagg atccaaatca aatccccaat 180
aatatccgtc gccaattgcc tcgttccatc acttcttcta catcttataa acgatttcct 240
ctctcccgtt gccgagctag gaattttcca gcaatgaggt ttggtggtag gattttgtat 300
agcaagactg ctactgaggt tgataagcga gcaatgcagc ttattaaagt tcttgatacc 360
aagagagatg aatctggaat agcttttgtt ggcttggata ttgagtggag accaagtttt 420
agaaaaggtg ttctcccggg gaaggttgcg actgtccaga tatgtgtaga tagtaattat 480
tgtgatgtta tgcatatttt tcattctggt atccctcaaa gtctccaaca tcttattgaa 540
gattcaacac ttgtaaaggt aggtattgga attgatggtg actctgtgaa gcttttccat 600
gactatggag ttagtatcaa agatgttgag gatctttcag atttagccaa ccaaaaaatt 660
ggtggagata aaaaatgggg ccttgcctca ctaactgaga cacttgtttg caaagagctc 720
ctgaagccaa acagaatcag gcttgggaac tgggagtttt atcctctgtc aaagcagcag 780
ttacaatacg cagcaacgga tgcttatgct tcatggcatc tttacaaggt aacaacaacg 840
aaaaaccatc ttctcacact caacgacctt gaagcaaaaa tctcacatcg ttctaattat 900
aatactgtta cttgtcgaaa acctggaggt tatcttcggt ga   942

<210> 2
<211> 313
<212> PRT
<213> Arabidopsis thaliana

<400> 2
Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
 1   5   10   15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
            20   25   30

1

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
    35   40   45

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
   50   55   60

Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
65   70   75   80

Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
          85   90   95

Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
          100   105   110

Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
          115   120   125

Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
          130   135   140

Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
145   150   155   160

Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
          165   170   175

His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
          180   185   190

Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
          195   200   205

Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
       210   215   220

Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
225   230   235   240

Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
          245   250   255

Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
          260   265   270

His Leu Tyr Lys Val Thr Thr Thr Lys Asn His Leu Leu Thr Leu Asn
          275   280   285

Asp Leu Glu Ala Lys Ile Ser His Arg Ser Asn Tyr Asn Thr Val Thr
          290   295   300

Cys Arg Lys Pro Gly Gly Tyr Leu Arg
305   310

<210> 3

2

<211> 1929
<212> DNA
<213> Arabidopsis thaliana

<400> 3
atgagatttg atgatcccat ggatgagttc aagaggaatc gaaagatgga ggaagattcg 60
aagaaggtaa tcgatgtgaa agtggctgag agtgataagg gattcgcgaa atttggcaag 120
gcagaggttc cgtttcatat accgacgtta acgaagcctc aagaggagta taagattttg 180
gtagacaatg ctaataatcc ttttgagcat gtttttgttgg agaagagtga agacggtctt 240
cggttcattc atccactgga ggaactatct gtgatggact ttgttgatag aaatctaagt 300
gagatgagac ctgttaagcc tctcccattg aagagactc cattcaagct agttgaagaa 360
gtcaaagatc ttgaggactt agctgctgca ttgcaaagtg ttgaagagtt tgctgtcgat 420
ctggagcata atcagtatag aactttttcaa ggattaacat gcttgatgca aatctctact 480
agaaccgagg attatattgt tgatatattc aagctttggg atcacattgg tccttatcta 540
agggaactct tcaaagaccc taaaaagaaa aaggtaatcc atggagcaga tcgagatatt 600
atttggcttc aacgggactt tggcatttat gtctgcaatc tttttgacac aggacaggct 660
tcaagggtgc taaagctgga gagaaatagt ctggaatttc ttctgaagca ttattgtgga 720
gttgctgcaa caaagaata ccaaaaagca gactggagaa taagacccct tccagatgta 780
atgaaaagat atgctagaga agatacacat tatctttgt acatttatga tgtaatgcga 840
atggagttgc acacaatggc aaaggaagat gagcaatctg actctcctct ggtagaggtg 900
tacaagcgca gttatgacgt gtgcatgcaa ctatatgaaa aagagctttg gactagggat 960
tcatatcttc acgtttatgg ggttcagaca ggtaatctca atgcggttca actttccatt 1020
gttgcgctgc aggggctttg tgaatggcgg gatcggattg cacgcgcaga tgatgagagc 1080
accggttatg tattgccaaa taaaactctt tttgacatag ccaaggagat gccaattgtt 1140
gttgcccagt tgcgccgttt gttgaagtca aagcttcctt acctcgagcg taattttgac 1200
gcagtgatca gtgtcatcag acgatcaatg caaaatgcag cggcattcga gccagttgtt 1260
caatctttga aagataggcg tcctgaaaca gtggttgaaa tgaatataga acctaagatt 1320
gagaaaacag acacaggagc ttcagcgtct tctctgagtc tggagaaggt ttgtgtggat 1380
gattcaaaga aacaaagcag tggttttgga gttttgccgt aaagaggaa gttggaaagt 1440
gacaaaacgg tggttgaaaa gaatatcgaa cctaagattg agaaaacagg cacagaagct 1500
tcagcttctt ctctgagttc gaagaaggtt tgtgtggatg attcaaagaa acaaagcagt 1560
ggttttggag ttttgctgtc aaagaggaag tttgaaagtg ataacaagaa gttgcaggta 1620
aaagaagagg tcaaagtgtc caagtccaag ccagataagg taatcatagt ggtggatgat 1680
gatgatgatg atgatgatga tgagtcttat gaacagagca cgaaagccgc tgatgctttg 1740
gacagagttt cggaaacgcc ttcgaaggga tcaccatcgt tgactcaaaa gccgaagaca 1800
tgtaatacag aggttattgt gttagacgat gatgatgact cggaaagcag agaagatgaa 1860
gacatgcgta ggagaagtga gaaacatagg agattcatga atatgaaacg tggctttctt 1920
aacatttag 1929

<210> 4
<211> 642
<212> PRT
<213> Arabidopsis thaliana

<400> 4
Met Arg Phe Asp Asp Pro Met Asp Glu Phe Lys Arg Asn Arg Lys Met
1   5   10   15

Glu Glu Asp Ser Lys Lys Val Ile Asp Val Lys Val Ala Glu Ser Asp
            20   25   30

Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
        35   40   45

Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
    50   55   60

3

```
Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
 65              70              75              80

Arg Phe Ile His Pro Leu Glu Glu Leu Ser Val Met Asp Phe Val Asp
             85              90              95

Arg Asn Leu Ser Glu Met Arg Pro Val Lys Pro Leu Pro Leu Glu Glu
            100             105             110

Thr Pro Phe Lys Leu Val Glu Glu Val Lys Asp Leu Glu Asp Leu Ala
            115             120             125

Ala Ala Leu Gln Ser Val Glu Glu Phe Ala Val Asp Leu Glu His Asn
            130             135             140

Gln Tyr Arg Thr Phe Gln Gly Leu Thr Cys Leu Met Gln Ile Ser Thr
145             150             155             160

Arg Thr Glu Asp Tyr Ile Val Asp Ile Phe Lys Leu Trp Asp His Ile
                165             170             175

Gly Pro Tyr Leu Arg Glu Leu Phe Lys Asp Pro Lys Lys Lys Lys Val
            180             185             190

Ile His Gly Ala Asp Arg Asp Ile Ile Trp Leu Gln Arg Asp Phe Gly
            195             200             205

Ile Tyr Val Cys Asn Leu Phe Asp Thr Gly Gln Ala Ser Arg Val Leu
            210             215             220

Lys Leu Glu Arg Asn Ser Leu Glu Phe Leu Leu Lys His Tyr Cys Gly
225             230             235             240

Val Ala Ala Asn Lys Glu Tyr Gln Lys Ala Asp Trp Arg Ile Arg Pro
            245             250             255

Leu Pro Asp Val Met Lys Arg Tyr Ala Arg Glu Asp Thr His Tyr Leu
            260             265             270

Leu Tyr Ile Tyr Asp Val Met Arg Met Glu Leu His Thr Met Ala Lys
            275             280             285

Glu Asp Glu Gln Ser Asp Ser Pro Leu Val Glu Val Tyr Lys Arg Ser
290             295             300

Tyr Asp Val Cys Met Gln Leu Tyr Glu Lys Glu Leu Trp Thr Arg Asp
305             310             315             320

Ser Tyr Leu His Val Tyr Gly Val Gln Thr Gly Asn Leu Asn Ala Val
            325             330             335

Gln Leu Ser Ile Val Ala Leu Gln Gly Leu Cys Glu Trp Arg Asp Arg
            340             345             350

Ile Ala Arg Ala Asp Asp Glu Ser Thr Gly Tyr Val Leu Pro Asn Lys
            355             360             365
```

4

Thr Leu Phe Asp Ile Ala Lys Glu Met Pro Ile Val Val Ala Gln Leu
    370   375   380

Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
385   390   395   400

Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
                405   410   415

Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
                420   425   430

Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
    435   440   445

Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
    450   455   460

Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
465   470   475   480

Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
                485   490   495

Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
                500   505   510

Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
            515   520   525

Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
    530   535   540

Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
545   550   555   560

Asp Asp Asp Asp Asp Asp Asp Glu Ser Tyr Glu Gln Ser Thr Lys Ala
            565   570   575

Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
            580   585   590

Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
            595   600   605

Asp Asp Asp Asp Asp Ser Glu Ser Arg Glu Asp Glu Asp Met Arg Arg
        610   615   620

Arg Ser Glu Lys His Arg Arg Phe Met Asn Met Lys Arg Gly Phe Leu
625   630   635   640

Asn Ile

<210> 5

<211> 714
<212> DNA
<213> Arabidopsis thaliana

<400> 5
atgaatttgc attttgattt ttggtgtttt atatttgaaa ctaatgcaga gaaaccttcg 60
aatggtcatc catatgaaac tgagatcact gttttgttag agaatcctca gattgagttt 120
ggattttttga gaggagagtg ttcattggaa atgagtgatt catatgtgtg ggttgagaca 180
gagtcgcagt taaaggaact tgcagaaata ttagcaaaag aacaagtttt tgcggttgac 240
actgagcagc atagtttgcg gtcgtttctt ggtttcactg ctctaattca gatttctaca 300
catgaggaag acttttttggt ggacacaatt gcgttacatg atgtaatgag tattcttcgt 360
cctgtttttct ctgatcctaa tatttgtaag gtgtttcacg gggctgacaa cgatgttatc 420
tggcttcaaa gagacttcca tatatatgtt gttaatatgt ttgatactgc caaggcatgt 480
gaagtgttgt caaagcctca acgatcactg catacttac ttgagacagt atgtggagtg 540
gctactaaca aattgctgca gcgtgaagat tggagacagc gtcctctgtc cgaagagatg 600
gtgcgatatg ctagaacaga tgcacactat ctgctttata ttgcagatag tttgacaact 660
gaactcaaac aattagccac tggtaggcat ctttgctatg gagaaacatt ttag 714

<210> 6
<211> 237
<212> PRT
<213> Arabidopsis thaliana

<400> 6
Met Asn Leu His Phe Asp Phe Trp Cys Phe Ile Phe Glu Thr Asn Ala
 1   5   10   15

Glu Lys Pro Ser Asn Gly His Pro Tyr Glu Thr Glu Ile Thr Val Leu
            20   25   30

Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
        35   40   45

Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
    50   55   60

Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
 65   70   75   80

Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
                85   90   95

Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
            100   105   110

His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
        115   120   125

Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
    130   135   140

Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
145   150   155   160

Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
                165   170   175

6

Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
            180   185   190

Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala
        195   200   205

His Tyr Leu Leu Tyr Ile Ala Asp Ser Leu Thr Thr Glu Leu Lys Gln
    210   215   220

Leu Ala Thr Gly Arg His Leu Cys Tyr Gly Glu Thr Phe
225   230   235

<210> 7
<211> 849
<212> DNA
<213> Arabidopsis thaliana

<400> 7
atgcagattg cattctctaa tgcaatatac ttggttgatg tcatcgaagg tggagaggtg 60
attatgaaag cgtgtaagcc tgcactcgag tctaattaca tcacgaaagt tattcacgat 120
tgcaagcgtg acagtgaggc tctatacttc cagtttggga taagattgca caatgttgtg 180
gacactcaga ttgcttattc tctgattgaa gaacaagaag ggcggaggag acctctagat 240
gattacatat cgtttgtttc actccttgct gatccacgtt actgcggtat atcctatgaa 300
gagaaagaag aagttcgagt tctcatgcgc caggacccaa agttttggac atacaggcct 360
atgactgagc tcatgatccg cgcagctgct gatgatgtcc gcttccttct gtatctctat 420
cacaaaatga tgggaaagct aaatcagcgg tcactatggc atcttgcagt tcgtggtgct 480
ttgtactgtc ggtgtctctg ctgcatgaat gatgctgatt ttgctgattg gccaaccgtt 540
cctccaattc cagtttttcct cgttaaggtc gtatatgctg tagagacaaa gaaaaaaaga 600
cgggtgacat tagcttcgat tgggttactg attgtagttg gactttttaaa tgtggcagat 660
aacctgaagt cagaagatca atgtcttgaa gaagagatcc tgtcagtgct tgatgttcca 720
ccaggaaaga tgggacgtgt gattggaagg aaaggagcat cgatcctcgc cattaaggaa 780
gcttgcaacg cggaaattct aattggaggg caaagggtc cacctgataa ggttagtctt 840
attccatag   849

<210> 8
<211> 282
<212> PRT
<213> Arabidopsis thaliana

<400> 8
Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
  1   5   10   15

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
            20   25   30

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
        35   40   45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
    50   55   60

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
 65   70   75   80

7

```
Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
                85                  90                      95

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
            100             105             110

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
        115             120             125

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
    130             135             140

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
145             150             155             160

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
            165             170             175

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
            180             185             190

Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
        195             200             205

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
    210             215             220

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
225             230             235             240

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
            245             250             255

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
        260             265             270

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
        275             280


<210> 9
<211> 720
<212> DNA
<213> Arabidopsis thaliana

<400> 9
atggctagga tcagaagaag aatccaaaag cgccatatcc acgaaaaccg ctacatcgat 60
ttctttggag aacgtttgat cgtcacggtc actcatacta cctcaaccat ccgccgttgg 120
attcatagca tccgtttctt cagccgtctt cgctcctcac accctctcgt tgttggactc 180
gacgtccaat ggacacccgg tggttccgat cctccaccgg atattctcca actatgtgtt 240
ggtaaccgct gtctcatcat ccagttgtct cactgtaaac gcattcctga ggtccttcga 300
agtttcttgg aagatgagac aatcactttt gtcggcgtct ggaacagcca agaccaggge 360
aagctcgaaa gattccgcca tcagttggag atatggagac ttctagacat aaggcactat 420
ctgcctacga ggctcctcaa tagttcgttt gagaagattg tagaggagtg tttggggtac 480
aagggagtga ggaaagataa ggagatatgt atgagtaatt ggggtgctcg tagcctttcc 540
catgatcaga ttgttcaggc gtcagatgat gtctatgttt gctgcaagct cggtgttaag 600
```

8

gaatgtatct ggaaagagcg ctcgaatgtt aaagaacgta tctggaaaga gagctcgaat 660
gttaaggaac atatctggaa agagagctcg aaactttatt ttgttggggt atgtttctga 720

<210> 10
<211> 239
<212> PRT
<213> Arabidopsis thaliana

<400> 10
Met Ala Arg Ile Arg Arg Arg Ile Gln Lys Arg His Ile His Glu Asn
 1   5   10   15

Arg Tyr Ile Asp Phe Phe Gly Glu Arg Leu Ile Val Thr Val Thr His
            20   25   30

Thr Thr Ser Thr Ile Arg Arg Trp Ile His Ser Ile Arg Phe Phe Ser
        35   40   45

Arg Leu Arg Ser Ser His Pro Leu Val Val Gly Leu Asp Val Gln Trp
    50   55   60

Thr Pro Gly Gly Ser Asp Pro Pro Asp Ile Leu Gln Leu Cys Val
 65   70   75   80

Gly Asn Arg Cys Leu Ile Ile Gln Leu Ser His Cys Lys Arg Ile Pro
                85   90   95

Glu Val Leu Arg Ser Phe Leu Glu Asp Glu Thr Ile Thr Phe Val Gly
            100   105   110

Val Trp Asn Ser Gln Asp Gln Gly Lys Leu Glu Arg Phe Arg His Gln
            115   120   125

Leu Glu Ile Trp Arg Leu Leu Asp Ile Arg His Tyr Leu Pro Thr Arg
    130   135   140

Leu Leu Asn Ser Ser Phe Glu Lys Ile Val Glu Glu Cys Leu Gly Tyr
145   150   155   160

Lys Gly Val Arg Lys Asp Lys Glu Ile Cys Met Ser Asn Trp Gly Ala
                165   170   175

Arg Ser Leu Ser His Asp Gln Ile Val Gln Ala Ser Asp Asp Val Tyr
            180   185   190

Val Cys Cys Lys Leu Gly Val Lys Glu Cys Ile Trp Lys Glu Arg Ser
            195   200   205

Asn Val Lys Glu Arg Ile Trp Lys Glu Ser Ser Asn Val Lys Glu His
    210   215   220

Ile Trp Lys Glu Ser Ser Lys Leu Tyr Phe Val Gly Val Cys Phe
225   230   235

<210> 11

9

<211> 654
<212> DNA
<213> Arabidopsis thaliana

<400> 11
atgaagagag gtatcaaaca tctatgtttc aatggcttca cgggctactc atcacttcat 60
catcattatc atgaacacca cgtcgacttc tttggagaac gtttgatcgt cacagtcact 120
catactccct cagtgatacg tcgatggatc cacagtatcc gcttcgtcag ccgtcttcgc 180
ttatcacacc ctctagttgt cggacttggc gttcaatgga caccccgtgg ttccgatcct 240
ccaccggata ttctccaact atgtgttggt actcgctgtc tcatcattca gttgtctcac 300
tgtaagtacg tccccgacgt ccttagaagt ttcttggaag atcagacaat cactttgtc 360
ggcgtatgga acagccaaga caaggacaag ctcgagagat ccaccatca gttggatatc 420
tggagacttg tccacataag gcactatctc catccgttgc tcttgagtag ctcgtttgag 480
acgattgtga aggtgtattt ggggcatgaa ggagtgacga aagataagga gttatgtatg 540
agtaattggg gtgctcgtag cctctctcat gatcagatag tacaagcgtc acatgatgtc 600
tatgtttgct gcaagctcgg tgttaaggaa cgtctctgga aatgggagc ttaa   654

<210> 12
<211> 217
<212> PRT
<213> Arabidopsis thaliana

<400> 12
Met Lys Arg Gly Ile Lys His Leu Cys Phe Asn Gly Phe Thr Gly Tyr
1   5   10   15

Ser Ser Leu His His His Tyr His Glu His His Val Asp Phe Phe Gly
            20   25   30

Glu Arg Leu Ile Val Thr Val Thr His Thr Pro Ser Val Ile Arg Arg
        35   40   45

Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
    50   55   60

Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
65   70   75   80

Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
                85   90   95

Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
            100   105   110

Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
            115   120   125

Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
    130   135   140

His Ile Arg His Tyr Leu His Pro Leu Leu Leu Ser Ser Ser Phe Glu
145   150   155   160

Thr Ile Val Lys Val Tyr Leu Gly His Glu Gly Val Thr Lys Asp Lys
                165   170   175

10

```
Glu Leu Cys Met Ser Asn Trp Gly Ala Arg Ser Leu Ser His Asp Gln
          180                 185                 190

Ile Val Gln Ala Ser His Asp Val Tyr Val Cys Cys Lys Leu Gly Val
          195                 200                 205

Lys Glu Arg Leu Trp Lys Met Gly Ala
    210                 215
```

<210> 13
<211> 261
<212> DNA
<213> Arabidopsis thaliana

<400> 13
```
atgatcaagt cgatcgagag ctttattgct cgttatgttt tccaagctac attatacaca 60
atctggtgcg aacgaaatgg cagaaggcat ggagagagag aggccgaacc agccgctctt 120
ctaataaaat tgattgataa gcaagccatc tttcctcaat cagagcaact gatgatctac 180
gctatgacaa gagcctccaa atctggtttg catcgagtgg ttgaaatcaa accatctata 240
gttcatgtgt ttaaccttta a                                           261
```

<210> 14
<211> 86
<212> PRT
<213> Arabidopsis thaliana

<400> 14
```
Met Ile Lys Ser Ile Glu Ser Phe Ile Ala Arg Tyr Val Phe Gln Ala
  1               5                  10                  15

Thr Leu Tyr Thr Ile Trp Cys Glu Arg Asn Gly Arg Arg His Gly Glu
              20                  25                  30

Arg Glu Ala Glu Pro Ala Ala Leu Leu Ile Lys Leu Ile Asp Lys Gln
          35                  40                  45

Ala Ile Phe Pro Gln Ser Glu Gln Leu Met Ile Tyr Ala Met Thr Arg
      50                  55                  60

Ala Ser Lys Ser Gly Leu His Arg Val Val Glu Ile Lys Pro Ser Ile
 65                  70                  75                  80

Val His Val Phe Asn Leu
                  85
```

<210> 15
<211> 2733
<212> DNA
<213> C. elegans

<400> 15
```
atggaagaag aaccgtacaa aagaaagcta acgaaagccg agaaaaaggc aaaatatcga 60
acagactacg ccgaaccgtt gaagtcacgc cgggaagttc tgaaagcaat tatgaatgga 120
cccgagtctg agcgggagag aaaagttcga gccaaaaatc gagaattttt caacgaggac 180
```

```
tatagatcag gagtcaacat ctacggaatg gctgtggata tgatgaaagc gatgccggat 240
agaggaaaaa catcgggaca aagtttggcg gtttggtatc tggaggattt tggagtttgg 300
ttaaaagagt cgggacagga gacggagctc agacagaaat atctgactgg aactattcaa 360
ataaacgcct tagatgtgtg cacaattgga caaaagcagc ttctcagtga aatcttcgat 420
atcaccaaag agaaattcac tgaggacatt acacagttgc tagatgctgc catcaagaaa 480
caagacttct ccgttgctgc agatatggct attcagtaca atcttctacg ggatcatcat 540
ttcgaacatc ttgttcttcc attaatgcta tctggcaaag atcaaacggc ttataaattg 600
ataagtaaca atgagaggat gcaacagcag cttgtagagt ttttttgatcg aatggttgga 660
atctcagtgg ttgccgttga agagatgctg aaaccctaca aggaaaccaa aattatgacg 720
attcctatgg agaaattgac gggaaaaacg ttggacaaac tcatttcgac gattatcaac 780
aaaaatactc acgaatacaa cttctccagg gaattgtcga agttcgccaa aaaccactca 840
cagaatggga atctgaaggc attgaagttt aatatcagtg aacgatacga gaagggaaaa 900
tccgatgaca actatttcca gcatatggtt gaaactttta ccaaagccga agatgttcgt 960
gaacctattt tgttttactt gtggagctca aatgacaccg agaaacaaat agatgccatc 1020
tgctttgcta tctacttagg aatcgctagt tccagcagct atcaactgcc gaatgttatg 1080
agggacttct ttcgacaacc tgattcgaag ctcagagaag caaaagaact tctagtgaga 1140
agaaaaacac tgcaagttcc tctaaatggc gaacaattat tcgtatttga gaatgagcga 1200
agaactcaaa tccacatggt gaaaactgaa tctgagatga attacttatg ttccgagatc 1260
aaatcactaa gcgacgagcc agcacctgtt tacgttggat tcgattctga gtggaaaccg 1320
tcgaatctta cagctgttca tgactcgaaa attgctatca tacaattgtt cttcaaaaat 1380
tgtgtatggc ttgtggattg cgtagaatta gaaaaggcaa atatggcaga tgactggtgg 1440
caaaagttcg catctcgatt gttcggagat tctcctgtaa aagtcgtagg atttgatatg 1500
aggaacgatc tggatgcaat ggctacaatc ccagcactga agtcatccat gaagatagaa 1560
gataccaaaa atgcattcga tctgaagcga ttagcagaga atgtttgcga tatcgacatg 1620
gaaattttag agctgccaaa gaagactttc aaattggcag atttgacaca ttatctactg 1680
ggattggagc tcgacaaaac tgaacaatgc agtaactggc aatgtcgtcc tctgcgaaaa 1740
aaacaaattg tgtacgcagc attggacgca gttgtcgtgg tggaaacatt caagaaaatc 1800
ttgtcgattg tagaggagaa aaacaaggac gcagatatcg agaagattgt cagagaatca 1860
aatgtaatgg ctccgaaaaa agacaaagga cacaaatcgt accgcaagct gaaaactatt 1920
ccatggcttg agctctacga tatcttgcga agccatcgta atcctacgag atcaccacag 1980
cgaccacacg acattaaagt tattgttgac acaatgctga ttggatttgg aaagaatctg 2040
aggagagttg gaattgatgt tattcttcca aaagacgtga gcgacttccg aaagtacctg 2100
aaggaaattg aacgagttgg cggcgagcat ctacgtcata taatcacagt gccatcgaaa 2160
agttacgaag ccttgaaaat ggattatgat aattatacaa ttgcaattcc ggaactcaat 2220
aacatgtctc ccgtagatca gcttattgag tttttcgacc tgttcaacgt agatattcgt 2280
ccggaagacg tatatcctcg atgcactgaa tgcaattctc ggcttcaaat taaattcccc 2340
ggaccagttt acatttctt gcaccaatac tgtgtcatcc atgtgcaaaa tgtttatcgt 2400
gcggatatga gcgaatttcc actggaagaa tggtggaatc gtatgcttca tatcaatcca 2460
gacgactacg acggagtaaa agtggaaatg tcgcgaccat ctccaacaag caagtggatc 2520
gtggcaactg ttcccacagg atgcctacat attacgcgac aaactgcact tcacaccaat 2580
ctgccagatg gaattgaagt tcgaatccac aaagtgcctg atgacgagtt caagcgtcga 2640
aatctcagct tctatgtgtg tggagaatgc ggtacggtgg cttgtgatgg tcgtggcaat 2700
caagcgtcgg agagcaccag ccaggaatgt tga                               2733


<210> 16
<211> 910
<212> PRT
<213> C. elegans

<400> 16
Met Glu Glu Glu Pro Tyr Lys Arg Lys Leu Thr Lys Ala Glu Lys Lys
  1               5                   10                  15

Ala Lys Tyr Arg Thr Asp Tyr Ala Glu Pro Leu Lys Ser Arg Arg Glu
            20                  25                  30
```

12

```
Val Leu Lys Ala Ile Met Asn Gly Pro Glu Ser Glu Arg Glu Arg Lys
        35                      40                  45

Val Arg Ala Lys Asn Arg Glu Phe Phe Asn Glu Asp Tyr Arg Ser Gly
    50                      55                  60

Val Asn Ile Tyr Gly Met Ala Val Asp Met Met Lys Ala Met Pro Asp
65                      70                  75                  80

Arg Gly Lys Thr Ser Gly Gln Ser Leu Ala Val Trp Tyr Leu Glu Asp
                85                  90                  95

Phe Gly Val Trp Leu Lys Glu Ser Gly Gln Glu Thr Glu Leu Arg Gln
                100                 105                 110

Lys Tyr Leu Thr Gly Thr Ile Gln Ile Asn Ala Leu Asp Val Cys Thr
        115                 120                 125

Ile Gly Gln Lys Gln Leu Leu Ser Glu Ile Phe Asp Ile Thr Lys Glu
    130                 135                 140

Lys Phe Thr Glu Asp Ile Thr Gln Leu Leu Asp Ala Ala Ile Lys Lys
145                 150                 155                 160

Gln Asp Phe Ser Val Ala Ala Asp Met Ala Ile Gln Tyr Asn Leu Leu
                165                 170                 175

Arg Asp His His Phe Glu His Leu Val Leu Pro Leu Met Leu Ser Gly
            180                 185                 190

Lys Asp Gln Thr Ala Tyr Lys Leu Ile Ser Asn Asn Glu Arg Met Gln
        195                 200                 205

Gln Gln Leu Val Glu Phe Phe Asp Arg Met Val Gly Ile Ser Val Val
    210                 215                 220

Ala Val Glu Glu Met Leu Lys Pro Tyr Lys Glu Thr Lys Ile Met Thr
225                 230                 235                 240

Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser
                245                 250                 255

Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu
                260                 265                 270

Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu
        275                 280                 285

Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn
        290                 295                 300

Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg
305                 310                 315                 320

Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln
                325                 330                 335
```

13

Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser
            340   345   350

Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp
            355   360   365

Ser Lys Leu Arg Glu Ala Lys Glu Leu Leu Val Arg Arg Lys Thr Leu
            370   375   380

Gln Val Pro Leu Asn Gly Glu Gln Leu Phe Val Phe Glu Asn Glu Arg
385   390   395   400

Arg Thr Gln Ile His Met Val Lys Thr Glu Ser Glu Met Asn Tyr Leu
            405   410   415

Cys Ser Glu Ile Lys Ser Leu Ser Asp Glu Pro Ala Pro Val Tyr Val
            420   425   430

Gly Phe Asp Ser Glu Trp Lys Pro Ser Asn Leu Thr Ala Val His Asp
            435   440   445

Ser Lys Ile Ala Ile Ile Gln Leu Phe Phe Lys Asn Cys Val Trp Leu
            450   455   460

Val Asp Cys Val Glu Leu Glu Lys Ala Asn Met Ala Asp Asp Trp Trp
465   470   475   480

Gln Lys Phe Ala Ser Arg Leu Phe Gly Asp Ser Pro Val Lys Val Val
            485   490   495

Gly Phe Asp Met Arg Asn Asp Leu Asp Ala Met Ala Thr Ile Pro Ala
            500   505   510

Leu Lys Ser Ser Met Lys Ile Glu Asp Thr Lys Asn Ala Phe Asp Leu
            515   520   525

Lys Arg Leu Ala Glu Asn Val Cys Asp Ile Asp Met Glu Ile Leu Glu
            530   535   540

Leu Pro Lys Lys Thr Phe Lys Leu Ala Asp Leu Thr His Tyr Leu Leu
545   550   555   560

Gly Leu Glu Leu Asp Lys Thr Glu Gln Cys Ser Asn Trp Gln Cys Arg
            565   570   575

Pro Leu Arg Lys Lys Gln Ile Val Tyr Ala Ala Leu Asp Ala Val Val
            580   585   590

Val Val Glu Thr Phe Lys Lys Ile Leu Ser Ile Val Glu Glu Lys Asn
            595   600   605

Lys Asp Ala Asp Ile Glu Lys Ile Val Arg Glu Ser Asn Val Met Ala
            610   615   620

Pro Lys Lys Asp Lys Gly His Lys Ser Tyr Arg Lys Leu Lys Thr Ile
625   630   635   640

14

Pro Trp Leu Glu Leu Tyr Asp Ile Leu Arg Ser His Arg Asn Pro Thr
                  645   650   655

Arg Ser Pro Gln Arg Pro His Asp Ile Lys Val Ile Val Asp Thr Met
              660   665   670

Leu Ile Gly Phe Gly Lys Asn Leu Arg Arg Val Gly Ile Asp Val Ile
          675   680   685

Leu Pro Lys Asp Val Ser Asp Phe Arg Lys Tyr Leu Lys Glu Ile Glu
      690   695   700

Arg Val Gly Gly Glu His Leu Arg His Ile Ile Thr Val Pro Ser Lys
705   710   715   720

Ser Tyr Glu Ala Leu Lys Met Asp Tyr Asp Asn Tyr Thr Ile Ala Ile
              725   730   735

Pro Glu Leu Asn Asn Met Ser Pro Val Asp Gln Leu Ile Glu Phe Phe
              740   745   750

Asp Leu Phe Asn Val Asp Ile Arg Pro Glu Asp Val Tyr Pro Arg Cys
          755   760   765

Thr Glu Cys Asn Ser Arg Leu Gln Ile Lys Phe Pro Gly Pro Val Leu
      770   775   780

His Phe Leu His Gln Tyr Cys Val Ile His Val Gln Asn Val Tyr Arg
785   790   795   800

Ala Asp Met Ser Glu Phe Pro Leu Glu Glu Trp Trp Asn Arg Met Leu
              805   810   815

His Ile Asn Pro Asp Asp Tyr Asp Gly Val Lys Val Glu Met Ser Arg
              820   825   830

Pro Ser Pro Thr Ser Lys Trp Ile Val Ala Thr Val Pro Thr Gly Cys
          835   840   845

Leu His Ile Thr Arg Gln Thr Ala Leu His Thr Asn Leu Pro Asp Gly
      850   855   860

Ile Glu Val Arg Ile His Lys Val Pro Asp Asp Glu Phe Lys Arg Arg
865   870   875   880

Asn Leu Ser Phe Tyr Val Cys Gly Glu Cys Gly Thr Val Ala Cys Asp
              885   890   895

Gly Arg Gly Asn Gln Ala Ser Glu Ser Thr Ser Gln Glu Cys
          900   905   910

<210> 17
<211> 4299
<212> DNA
<213> Homo sapiens

15

<400> 17

```
atgagtgaaa aaaaattgga aacaactgca cagcagcgga aatgtcctga atggatgaat 60
gtgcagaata aaagatgtgc tgtagaagaa agaaaggcat gtgttcggaa gagtgttttt 120
gaagatgacc tccccttctt agaattcact ggatccattg tgtatagtta cgatgctagt 180
gattgctctt tcctgtcaga agatattagc atgagtctat cagatgggga tgtggtggga 240
tttgacatgg agtggccacc attatacaat agagggaaac ttggcaaagt tgcactaatt 300
cagttgtgtg tttctgagag caaatgttac ttgttccacg tttcttccat gtcagttttt 360
ccccagggat taaaaatgtt gcttgaaaat aaagcagtta aaaaggcagg tgtaggaatt 420
gaaggagatc agtggaaact tctacgtgac tttgatatca aattgaagaa ttttgtggag 480
ttgacagatg ttgccaataa aaagctgaaa tgtacagaga cctggagcct taacagtctg 540
gttaaacacc tcttaggtaa acagctcctg aaagacaagt ctatccgctg tagcaattgg 600
agtaaatttc ctctcactga ggaccagaaa ctgtatgcag ccactgatgc ttatgctggt 660
tttattattt accgaaattt agagattttg gatgatactg tgcaaaggtt tgctataaat 720
aaagaggaag aaatcctact tagcgacatg aacaaacagt tgacttcaat ctctgaggaa 780
gtgatggatc tggctaagca tcttcctcat gctttcagta aattggaaaa cccacggagg 840
gtttctatct tactaaagga tatttcagaa aatctatatt cactgaggag gatgataatt 900
gggtctacta acattgagac tgaactgagg cccagcaata atttaaactt attatccttt 960
gaagattcaa ctactggggg agtacaacag aaacaaatta gagaacatga agttttaatt 1020
cacgttgaag atgaaacatg ggacccaaca cttgatcatt tagctaaaca tgatggagaa 1080
gatgtacttg gaaataaagt ggaacgaaaa gaagatggat ttgaagatgg agtagaagac 1140
aacaaattga aagagaatat ggaaagagct tgtttgatgt cgttagatat tacagaacat 1200
gaactccaaa ttttggaaca gcagtctcag gaagaatatc ttagtgatat tgcttataaa 1260
tctactgagc atttatctcc caatgataat gaaaacgata cgtcctatgt aattgagagt 1320
gatgaagatt tagaaatgga gatgcttaag catttatctc ccaatgataa tgaaaacgat 1380
acgtcctatg taattgagag tgatgaagat ttagaaatgg agatgcttaa gtctttagaa 1440
aacctcaata gtggcacggt agaaccaact cattctaaat gcttaaaaat ggaaagaaat 1500
ctgggtcttc ctactaaaga agaagaagaa gatgatgaaa atgaagctaa tgaaggggaa 1560
gaagatgatg ataaggactt tttgtggcca gcacccaatg aagagcaagt tacttgcctc 1620
aagatgtact ttggccattc cagtttttaaa ccagttcagt ggaaagtgat tcattcagta 1680
ttagaagaaa gaagagataa tgttgctgtc atggcaactg gatatggaaa gagtttgtgc 1740
ttccagtatc cacctgttta tgtaggcaag attggccttg ttatctctcc ccttatttct 1800
ctgatggaag accaagtgct acagcttaaa atgtccaaca tcccagcttg cttccttgga 1860
tcagcacagt cagaaaatgt tctaacagat attaaattag gtaaataccg gattgtatac 1920
gtaactccag aatactgttc aggtaacatg ggcctgctcc agcaacttga ggctgatatt 1980
ggtatcacgc tcattgctgt ggatgaggct cactgtattt ctgagtgggg gcatgatttt 2040
agggattcat tcaggaagtt gggctcccta aagacagcac tgccaatggt tccaatcgtt 2100
gcacttactg ctactgcaag ttcttcaatc cgggaagaca ttgtacgttg cttaaatctg 2160
agaaatcctc agatcacctg tactggtttt gatcgaccaa acctgtattt agaagttagg 2220
cgaaaaacag gaatatcct tcaggatctg cagccatttc ttgtcaaaac aagttcccac 2280
tgggaatttg aaggtccaac aatcatctac tgtccttcta gaaaaatgac acaacaagtt 2340
acaggtgaac ttaggaaact taatctatcc tgtggaacat accatgcggg catgagtttt 2400
agcacaagga agacattca tcataggttt gtaagagatg aaaattcagtg tgtcatagct 2460
accatagctt ttggaatggg cattaataaa gctgacattc gccaagtcat tcattacggt 2520
gctcctaagg acatggaatc atattatcag gagattggta gagctggtcg tgatggactt 2580
caaagttctt gtcacgtcct ctgggctcct gcagacatta acttaaatag gcaccttctt 2640
actgagatac gtaatgagaa gtttcgatta tacaaattaa agatgatggc aaagatggaa 2700
aaatatcttc attctagcag atgtaggaga caaatcatct tgtctcattt tgaggacaaa 2760
caagtacaaa aagcctcctt gggaattatg ggaactgaaa aatgctgtga taattgcagg 2820
tccagattgg atcattgcta ttccatggat gactcagagg atacatcctg ggactttggt 2880
ccacaagcat ttaagctttt gtctgctgtg gacatcttag gcgaaaaatt tggaattggg 2940
cttccaattt tatttctccg aggatctaat tctcagcgtc ttgccgatca atatcgcagg 3000
cacagtttat ttggcactgg caaggatcaa acagagagtt ggtggaaggc tttttcccgt 3060
cagctgatca ctgagggatt cttggtagaa gtttctcggt ataacaaatt tatgaagatt 3120
tgcgccctta cgaaaaaggg tagaaattgg cttcataaag ctaatacaga atctcagagc 3180
ctcatccttc aagctaatga agaattgtgt ccaaagaagt ttcttctgcc tagttcgaaa 3240
actgtatctt cgggcaccaa agagcattgt tataatcaag taccagttga attaagtaca 3300
gagaagaagt ctaacttgga gaagttatat tcttataaac catgtgataa gatttcttct 3360
```

16

```
gggagtaaca tttctaaaaa aagtatcatg gtacagtcac cagaaaaagc ttacagttcc 3420
tcacagcctg ttatttcggc acaagagcag gagactcaga ttgtgttata tggcaaattg 3480
gtagaagcta ggcagaaaca tgccaataaa atggatgttc ccccagctat tctggcaaca 3540
aacaagatac tggtggatat ggccaaaatg agaccaacta cggttgaaaa cgtaaaaagg 3600
attgatggtg tttctgaagg caaagctgcc atgttggccc ctctgttgga agtcatcaaa 3660
catttctgcc aaacaaatag tgttcagaca gacctctttt caagtacaaa acctcaagaa 3720
gaacagaaga cgagtctggt agcaaaaaat aaaatatgca cactttcaca gtctatggcc 3780
atcacatact ctttattcca agaaaagaag atgcctttga gagcatagc tgagagcagg 3840
attctgcctc tcatgacaat tggcatgcac ttatcccaag cggtgaaagc tggctgcccc 3900
cttgatttgg agcgagcagg cctgactcca gaggttcaga agattattgc tgatgttatc 3960
cgaaaccctc ccgtcaactc agatatgagt aaaattagcc taatcagaat gttagttcct 4020
gaaaacattg acacgtacct tatccacatg gcaattgaga tccttaaaca tggtcctgac 4080
agcggacttc aaccttcatg tgatgtcaac aaaaggagat gttttcccgg ttctgaagag 4140
atctgttcaa gttctaagag aagcaaggaa gaagtaggca tcaatactga gacttcatct 4200
gcagagagaa agagacgatt acctgtgtgg tttgccaaag gaagtgatac cagcaagaaa 4260
ttaatggaca aaacgaaaag gggaggtctt tttagttaa            4299


<210> 18
<211> 1432
<212> PRT
<213> Homo sapiens

<400> 18
Met Ser Glu Lys Lys Leu Glu Thr Thr Ala Gln Gln Arg Lys Cys Pro
 1               5                   10                  15

Glu Trp Met Asn Val Gln Asn Lys Arg Cys Ala Val Glu Glu Arg Lys
                20                  25                  30

Ala Cys Val Arg Lys Ser Val Phe Glu Asp Asp Leu Pro Phe Leu Glu
            35                  40                  45

Phe Thr Gly Ser Ile Val Tyr Ser Tyr Asp Ala Ser Asp Cys Ser Phe
     50                  55                  60

Leu Ser Glu Asp Ile Ser Met Ser Leu Ser Asp Gly Asp Val Val Gly
 65                  70                  75                  80

Phe Asp Met Glu Trp Pro Pro Leu Tyr Asn Arg Gly Lys Leu Gly Lys
                 85                  90                  95

Val Ala Leu Ile Gln Leu Cys Val Ser Glu Ser Lys Cys Tyr Leu Phe
                100                 105                 110

His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
            115                 120                 125

Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
    130                 135                 140

Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
145                 150                 155                 160

Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
                165                 170                 175
```

17

```
Leu Asn Ser Leu Val Lys His Leu Leu Gly Lys Gln Leu Leu Lys Asp
        180                 185                 190

Lys Ser Ile Arg Cys Ser Asn Trp Ser Lys Phe Pro Leu Thr Glu Asp
        195                 200                 205

Gln Lys Leu Tyr Ala Ala Thr Asp Ala Tyr Ala Gly Phe Ile Ile Tyr
    210                 215                 220

Arg Asn Leu Glu Ile Leu Asp Asp Thr Val Gln Arg Phe Ala Ile Asn
225                 230                 235                 240

Lys Glu Glu Glu Ile Leu Leu Ser Asp Met Asn Lys Gln Leu Thr Ser
        245                 250                 255

Ile Ser Glu Glu Val Met Asp Leu Ala Lys His Leu Pro His Ala Phe
        260                 265                 270

Ser Lys Leu Glu Asn Pro Arg Arg Val Ser Ile Leu Leu Lys Asp Ile
        275                 280                 285

Ser Glu Asn Leu Tyr Ser Leu Arg Arg Met Ile Ile Gly Ser Thr Asn
    290                 295                 300

Ile Glu Thr Glu Leu Arg Pro Ser Asn Asn Leu Asn Leu Leu Ser Phe
305                 310                 315                 320

Glu Asp Ser Thr Thr Gly Gly Val Gln Gln Lys Gln Ile Arg Glu His
        325                 330                 335

Glu Val Leu Ile His Val Glu Asp Glu Thr Trp Asp Pro Thr Leu Asp
        340                 345                 350

His Leu Ala Lys His Asp Gly Glu Asp Val Leu Gly Asn Lys Val Glu
        355                 360                 365

Arg Lys Glu Asp Gly Phe Glu Asp Gly Val Glu Asp Asn Lys Leu Lys
        370                 375                 380

Glu Asn Met Glu Arg Ala Cys Leu Met Ser Leu Asp Ile Thr Glu His
385                 390                 395                 400

Glu Leu Gln Ile Leu Glu Gln Gln Ser Gln Glu Glu Tyr Leu Ser Asp
            405                 410                 415

Ile Ala Tyr Lys Ser Thr Glu His Leu Ser Pro Asn Asp Asn Glu Asn
        420                 425                 430

Asp Thr Ser Tyr Val Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met
        435                 440                 445

Leu Lys His Leu Ser Pro Asn Asp Asn Glu Asn Asp Thr Ser Tyr Val
    450                 455                 460

Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met Leu Lys Ser Leu Glu
465                 470                 475                 480
```

18

```
Asn Leu Asn Ser Gly Thr Val Glu Pro Thr His Ser Lys Cys Leu Lys
            485                 490                 495

Met Glu Arg Asn Leu Gly Leu Pro Thr Lys Glu Glu Glu Asp Asp
            500                 505                 510

Glu Asn Glu Ala Asn Glu Gly Glu Glu Asp Asp Asp Lys Asp Phe Leu
            515                 520                 525

Trp Pro Ala Pro Asn Glu Glu Gln Val Thr Cys Leu Lys Met Tyr Phe
    530                 535                 540

Gly His Ser Ser Phe Lys Pro Val Gln Trp Lys Val Ile His Ser Val
545                 550                 555                 560

Leu Glu Glu Arg Arg Asp Asn Val Ala Val Met Ala Thr Gly Tyr Gly
                565                 570                 575

Lys Ser Leu Cys Phe Gln Tyr Pro Pro Val Tyr Val Gly Lys Ile Gly
            580                 585                 590

Leu Val Ile Ser Pro Leu Ile Ser Leu Met Glu Asp Gln Val Leu Gln
            595                 600                 605

Leu Lys Met Ser Asn Ile Pro Ala Cys Phe Leu Gly Ser Ala Gln Ser
    610                 615                 620

Glu Asn Val Leu Thr Asp Ile Lys Leu Gly Lys Tyr Arg Ile Val Tyr
625                 630                 635                 640

Val Thr Pro Glu Tyr Cys Ser Gly Asn Met Gly Leu Leu Gln Gln Leu
            645                 650                 655

Glu Ala Asp Ile Gly Ile Thr Leu Ile Ala Val Asp Glu Ala His Cys
            660                 665                 670

Ile Ser Glu Trp Gly His Asp Phe Arg Asp Ser Phe Arg Lys Leu Gly
    675                 680                 685

Ser Leu Lys Thr Ala Leu Pro Met Val Pro Ile Val Ala Leu Thr Ala
    690                 695                 700

Thr Ala Ser Ser Ser Ile Arg Glu Asp Ile Val Arg Cys Leu Asn Leu
705                 710                 715                 720

Arg Asn Pro Gln Ile Thr Cys Thr Gly Phe Asp Arg Pro Asn Leu Tyr
                725                 730                 735

Leu Glu Val Arg Arg Lys Thr Gly Asn Ile Leu Gln Asp Leu Gln Pro
            740                 745                 750

Phe Leu Val Lys Thr Ser Ser His Trp Glu Phe Glu Gly Pro Thr Ile
            755                 760                 765

Ile Tyr Cys Pro Ser Arg Lys Met Thr Gln Gln Val Thr Gly Glu Leu
    770                 775                 780
```

19

Arg Lys Leu Asn Leu Ser Cys Gly Thr Tyr His Ala Gly Met Ser Phe
785   790   795   800

Ser Thr Arg Lys Asp Ile His His Arg Phe Val Arg Asp Glu Ile Gln
                805   810   815

Cys Val Ile Ala Thr Ile Ala Phe Gly Met Gly Ile Asn Lys Ala Asp
                820   825   830

Ile Arg Gln Val Ile His Tyr Gly Ala Pro Lys Asp Met Glu Ser Tyr
        835   840   845

Tyr Gln Glu Ile Gly Arg Ala Gly Arg Asp Gly Leu Gln Ser Ser Cys
    850   855   860

His Val Leu Trp Ala Pro Ala Asp Ile Asn Leu Asn Arg His Leu Leu
865   870   875   880

Thr Glu Ile Arg Asn Glu Lys Phe Arg Leu Tyr Lys Leu Lys Met Met
                885   890   895

Ala Lys Met Glu Lys Tyr Leu His Ser Ser Arg Cys Arg Arg Gln Ile
            900   905   910

Ile Leu Ser His Phe Glu Asp Lys Gln Val Gln Lys Ala Ser Leu Gly
        915   920   925

Ile Met Gly Thr Glu Lys Cys Cys Asp Asn Cys Arg Ser Arg Leu Asp
    930   935   940

His Cys Tyr Ser Met Asp Asp Ser Glu Asp Thr Ser Trp Asp Phe Gly
945   950   955   960

Pro Gln Ala Phe Lys Leu Leu Ser Ala Val Asp Ile Leu Gly Glu Lys
                965   970   975

Phe Gly Ile Gly Leu Pro Ile Leu Phe Leu Arg Gly Ser Asn Ser Gln
            980   985   990

Arg Leu Ala Asp Gln Tyr Arg Arg His Ser Leu Phe Gly Thr Gly Lys
        995   1000   1005

Asp Gln Thr Glu Ser Trp Trp Lys Ala Phe Ser Arg Gln Leu Ile Thr
    1010   1015   1020

Glu Gly Phe Leu Val Glu Val Ser Arg Tyr Asn Lys Phe Met Lys Ile
1025   1030   1035   1040

Cys Ala Leu Thr Lys Lys Gly Arg Asn Trp Leu His Lys Ala Asn Thr
                1045   1050   1055

Glu Ser Gln Ser Leu Ile Leu Gln Ala Asn Glu Glu Leu Cys Pro Lys
            1060   1065   1070

Lys Phe Leu Leu Pro Ser Ser Lys Thr Val Ser Ser Gly Thr Lys Glu
        1075   1080   1085

20

His Cys Tyr Asn Gln Val Pro Val Glu Leu Ser Thr Glu Lys Lys Ser
   1090   1095   1100

Asn Leu Glu Lys Leu Tyr Ser Tyr Lys Pro Cys Asp Lys Ile Ser Ser
1105   1110   1115   1120

Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys
              1125   1130   1135

Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr
           1140   1145   1150

Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala
           1155   1160   1165

Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu
   1170   1175   1180

Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg
1185   1190   1195   1200

Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu
              1205   1210   1215

Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu
           1220   1225   1230

Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala
           1235   1240   1245

Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser
   1250   1255   1260

Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg
1265   1270   1275   1280

Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys
              1285   1290   1295

Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val
           1300   1305   1310

Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp
           1315   1320   1325

Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp
   1330   1335   1340

Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp
1345   1350   1355   1360

Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro
           1365   1370   1375

Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val
           1380   1385   1390

21

Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro
      1395   1400   1405

Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys
    1410   1415   1420

Thr Lys Arg Gly Gly Leu Phe Ser
1425   1430

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220> Misc_feature
<223> 1...30

<400> 19
cgacatgatc tgatacatcg ttatgccatt   30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220> Misc_feature
<223> 1...29

<400> 20
cattttataa taacgctgcg gacatctac   29

<210> 21
<211> 1041
<212> DNA
<213> Arabidopsis thaliana

<400> 21
atgtttgagt ttttcgcttc aggaggaagg tcgccgacac aagaagctaa tgagccacca 60
gttccgattt acattgtgac ggatccgttt caacttcctg ctgatttcct aaacccttct 120
cctgaaaaga aattggttat cggttttgac tgtgagggtg ttgacctctg ccgacatggg 180
aaactttgta tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240
ggtggagagg tgattatgaa agcgtgtaag cctgcactcg agtctaatta catcacgaaa 300
gttattcacg attgcaagcg tgacagtgag gctctatact ccagtttggg ataagattg 360
cacaatgttg tggacactca gattgcttat tctctgattg aagaacaaga agggcggagg 420
agacctctag atgattacat atcgtttgtt tcactccttg ctgatccacg ttactgcggt 480
atatcctatg aagagaaaga agaagttcga gttctcatgc gccaggaccc aaagttttgg 540
acatacaggc ctatgactga gctcatgatc cgcgcagctg ctgatgatgt ccgcttcctt 600
ctgtatctct atcacaaaat gatgggaaag ctaaatcagc ggtcactatg gcatcttgca 660
gttcgtggtg ctttgtactg tcggtgtctc tgctgcatga atgatgctga ttttgctgat 720
tggccaaccg ttcctccaat tccagttttc ctcgttaagg tcgtatatgc tgtagagaca 780
aagaaaaaa gacgggtgac attagcttcg attgggttac tgattgtagt tggactttta 840
aatgtggcag ataacctgaa gtcagaagat caatgtcttg aagaagagat cctgtcagtg 900
cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960
gccattaagg aagcttgcaa cgcggaaatt ctaattggag gggcaaaggg tccacctgat 1020

22

aaggttagtc ttattccata g   1041

<210> 22
<211> 346
<212> PRT
<213> Arabidopsis thaliana

<400> 22
Met Phe Glu Phe Phe Ala Ser Gly Gly Arg Ser Pro Thr Gln Glu Ala
 1   5   10   15

Asn Glu Pro Pro Val Pro Ile Tyr Ile Val Thr Asp Pro Phe Gln Leu
             20   25   30

Pro Ala Asp Phe Leu Asn Pro Ser Pro Glu Lys Lys Leu Val Ile Gly
         35   40   45

Phe Asp Cys Glu Gly Val Asp Leu Cys Arg His Gly Lys Leu Cys Ile
     50   55   60

Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
65   70   75   80

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
                 85   90   95

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
             100   105   110

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
         115   120   125

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
     130   135   140

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
145   150   155   160

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
                 165   170   175

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
             180   185   190

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
         195   200   205

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
     210   215   220

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
225   230   235   240

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
                 245   250   255

23

```
Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
            260                 265             270

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
            275             280             285

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
    290             295             300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
305             310             315             320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
            325             330             335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
            340             345


<210> 23
<211> 1049
<212> DNA
<213> Arabidopsis thaliana

<400> 23
accaaagcat taattttttat tttttttgttt cagtaaaaga aatgtcatcg tcaaattgga    60
tcgacgacgc ttttacagag gaagagcttc tcgctatcga cgccatcgaa gcttcctaca   120
atttctcccg ttcttcttct tcttcttcct ctgctgctcc gaccgtacaa gctacaacct   180
ccgtccatgg ccacgaggag gatccaaatc aaatccccaa taatatccgt cgccaattgc   240
ctcgttccat cacttcttct acatcttata aacgatttcc tctctcccgt tgccgagcta   300
ggaattttcc agcaatgagg tttggtggta ggattttgta tagcaagact gctactgagg   360
ttgataagcg agcaatgcag cttattaaag ttcttgatac caagagagat gaatctggaa   420
tagcttttgt tggcttggat attgagtgga gaccaagttt tagaaaaggt gttctcccgg   480
ggaaggttgc gactgtccag atatgtgtag atagtaatta ttgtgatgtt atgcatattt   540
ttcattctgg tatccctcaa agtctccaac atcttattga agattcaaca cttgtaaagg   600
taggtattgg aattgatggt gactctgtga agcttttcca tgactatgga gttagtatca   660
aagatgttga ggatctttca gatttagcca accaaaaaat tggtggagat aaaaaatggg   720
gccttgcctc actaactgag acacttgttt gcaaagagct cctgaagcca aacagaatca   780
ggcttgggaa ctggagtttt atcctctgt caaagcagca gttacaatac gcagcaacgg   840
atgcttatgc ttcatggcat ctttacaagg ttcttaagga ccttcctgat gctgtcagtg   900
gctcataacg tgaaggagga agcttaaagg ttagcctata accccaagag ttagcatcaa   960
atgatatgat acacctaatc tagtcaagta gatgcaattc ttgtgaatat tgtatctagt  1020
tctggtccct ttaaccgtcc agaaactag                                    1049


<210> 24
<211> 288
<212> PRT
<213> Arabidopsis thaliana

<400> 24
Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
1               5               10              15

Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
            20              25              30
```

24

```
Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
    35                  40                  45

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
    50                  55                  60

Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
65                  70                  75                  80

Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
            85                  90                  95

Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
            100                 105                 110

Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
        115                 120                 125

Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
    130                 135                 140

Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
145                 150                 155                 160

Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
            165                 170                 175

His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
            180                 185                 190

Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
        195                 200                 205

Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
    210                 215                 220

Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
225                 230                 235                 240

Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
            245                 250                 255

Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
        260                 265                 270

His Leu Tyr Lys Val Leu Lys Asp Leu Pro Asp Ala Val Ser Gly Ser
    275                 280                 285
```

<210> 25
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(22)

<223> Primer

<400> 25
ttcggaacca ccatcaaaca gg   22

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(22)
<223> Primer

<400> 26
ttgctgcaac tctctcaggg cc   22

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(21)
<223> Primer

<400> 27
tcagctgttg cccgtctcac t   21

<210> 28
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(16)
<223> n=a, c, g, or t

<400> 28
wgtgnagwan canaga   16

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(27)
<223> Primer

```
<400> 29
gctccgccca cataattcaa acaacac                                          27


<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(22)
<223> Primer

<400> 30
ttcgaaaaca ttacctccga tc                                              22


<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(25)
<223> Primer

<400> 31
ggcttttgca tttggtatct actag                                          25


<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(25)
<223> Primer

<400> 32
atgtcatcgt caaattggat cgacg                                          25



<210> 33
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(27)
<223> Primer

<400> 33
cgcttatcaa cctcagtagc agtcttg                                        27
```

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc_feature
<222> (1)..(24)
<223> Primer

<400> 34
ttatgagcca ctgacagcat cagg   24